SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: Artificial promoter libraries for selected
organisms and promoters derived from such libraries

(iii) NUMBER OF SEQUENCES: 58

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

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(vi) CURRENT APPLICATION DATA:
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(2) INFORMATION FOR SEQ ID NO: 1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 100 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:26..82
        (C) IDENTIFICATION METHOD: experimental
        (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
            /standard_name= "Artificial promoter library"
            /note= "A degenerated sequence specifying a mixture of
            artificial promoters covering a wide range of expression in
            small steps in L. lactis"

    (ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION:31..45
        (D) OTHER INFORMATION:/standard_name= "Consensus
            sequence"

    (ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION:60..69
        (D) OTHER INFORMATION:/standard_name= "Consensus
            sequence"

(ix) FEATURE:
    (A) NAME/KEY: misc_feature
    (B) LOCATION:74..82
    (D) OTHER INFORMATION:/standard_name= "Consensus
        sequence"

(ix) FEATURE:
    (A) NAME/KEY: -35_signal
    (B) LOCATION:40..45
    (D) OTHER INFORMATION:/standard_name= "-35 box"

(ix) FEATURE:
    (A) NAME/KEY: -10_signal
    (B) LOCATION:63..68
    (D) OTHER INFORMATION:/standard_name= "Pribnow box"

(ix) FEATURE:
    (A) NAME/KEY: misc_recomb
    (B) LOCATION:3..25
    (C) IDENTIFICATION METHOD: experimental
    (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
        /standard_name= "Multiple cloning site"
        /label= MCS
        /note= "A sequence specifying recognition sites for the
        restriction endonucleases: NlaIV, BstYI, BamHI, AlwI, MboI,
        DpnI, AflII, MseI, SspI, NsiI."

(ix) FEATURE:
    (A) NAME/KEY: misc_recomb
    (B) LOCATION:74..98
    (C) IDENTIFICATION METHOD: experimental
    (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
        /standard_name= "Multiple cloning site"
        /label= MCS
        /note= "A sequence specifying recognition sites for the
        restriction endonucleases: ScaI, RsaI, HpaI, HincII, MseI, SfcI,
        PstI, Fnu4HI, BbvI, PvuII, NspBII, AluI, EcoRI."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGGGATCCTT AAGAATATTA TGCATNNNNN AGTTTATTCT TGACANNNNN
NNNNNNNNNT   60

GGTATAATAN NANAGTACTG TTAACTGCAG CTGAATTCGG
100

(2) INFORMATION FOR SEQ ID NO: 2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:23..95
        (D) OTHER INFORMATION:/standard_name= "Artificial
            promoter library"
            /note= "A degenerated sequence specifying a mixture of
            artificial temperature regulated promoters covering a wide range
            of expression in small steps in L. lactis"

    (ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION:23..49
        (D) OTHER INFORMATION:/standard_name= "Sequence providing
            temperature regulation to promoters"
            /note= "This sequence comprising two inverted repeats separated
            by a short spacer provides temperature (heat shock) regulation
            to promoters in Gram-positive bacteria"

    (ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION:50..60
        (D) OTHER INFORMATION:/standard_name= "Consensus
            sequence"

    (ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION:75..84

(D) OTHER INFORMATION:/standard_name= "Consensus
    sequence"

(ix) FEATURE:
    (A) NAME/KEY: misc_feature
    (B) LOCATION:89..95
    (D) OTHER INFORMATION:/standard_name= "Consensus
        sequence"

(ix) FEATURE:
    (A) NAME/KEY: -35_signal
    (B) LOCATION:55..60
    (D) OTHER INFORMATION:/standard_name= "-35 box"

(ix) FEATURE:
    (A) NAME/KEY: -10_signal
    (B) LOCATION:78..83
    (D) OTHER INFORMATION:/standard_name= "Pribnow box"

(ix) FEATURE:
    (A) NAME/KEY: misc_recomb
    (B) LOCATION:3..22
    (D) OTHER INFORMATION:/standard_name= "Multiple cloning
        site"
        /label= MCS
        /note= "A sequence specifying recognition sites for the
        restriction endonucleases: NlaIV, BstYI, BamHI, AlwI, MboI,
        DpnI, HindIII, AluI, MseI (2 sites), SspI, AseI."

(ix) FEATURE:
    (A) NAME/KEY: misc_recomb
    (B) LOCATION:89..111
    (D) OTHER INFORMATION:/standard_name= "Multiple cloning
        site"
        /label= MCS
        /note= "A sequence specifying recognition sites for the
        restriction endonucleases: ScaI, RsaI, SfcI, PstI, Fnu4HI, BbvI,
        PvuII, NspBII, AluI, XbaI, MaeI, EcoRI, ApoI."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CGGGATCCAA GCTTAATATT AATTAGCACT CNNNNNNNNN GAGTGCTAAT
TTTTTTGACA   60

NNNNNNNNN NNNNTGGTAT AATANNANAG TACTGCAGCT GTCTAGAATT CGG   113

(2) INFORMATION FOR SEQ ID NO: 3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 199 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Saccharomyces cerevisiae

    (ix) FEATURE:
        (A) NAME/KEY: protein_bind
        (B) LOCATION:10..16
        (D) OTHER INFORMATION:/function= "Activating promoters in
            S. cerevisiae"
            /bound_moiety= "GCN4 protein"
            /standard_name= "Upstream activating sequence"
            /label= UAS_GCN4p
            /note= "A DNA sequence that specifies a binding site for the
            GCN4 protein, which activates the transcription of genes
            involved in aminoacid synthesis in S. cerevisiae."

    (ix) FEATURE:
        (A) NAME/KEY: TATA_signal
        (B) LOCATION:67..72
        (D) OTHER INFORMATION:/standard_name= "TATA box"

    (ix) FEATURE:
        (A) NAME/KEY: misc_signal
        (B) LOCATION:122..144
        (D) OTHER INFORMATION:/function= "Transcription
            initiation"
            /standard_name= "TI box"

    (ix) FEATURE:

(A) NAME/KEY: protein_bind
(B) LOCATION:122..144
(D) OTHER INFORMATION:/bound_moiety= "Arginine repressor"
/standard_name= "arginine repressor binding site"
/label= argR

(ix) FEATURE:
(A) NAME/KEY: misc_RNA
(B) LOCATION:145..192
(D) OTHER INFORMATION:/function= "Spacer"
/standard_name= "Part of native sequence for ARG8
gene incl. first codon"

(ix) FEATURE:
(A) NAME/KEY: misc_recomb
(B) LOCATION:3..8
(D) OTHER INFORMATION:/standard_name= "Recognition site
for restriction endonuclease EcoRI"
/label= EcoRI_site

(ix) FEATURE:
(A) NAME/KEY: misc_recomb
(B) LOCATION:192..197
(D) OTHER INFORMATION:/standard_name= "Recognition site
for restriction endonuclease BamHI"
/label= BamHI_site

(ix) FEATURE:
(A) NAME/KEY: promoter
(B) LOCATION:10..192
(D) OTHER INFORMATION:/standard_name= "Artificial
promoter library"
/note= "A degenerated sequence specifying a mixture of
artificial promoters covering a wide range of expression in
small steps in S. cerevisiae"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CAGAATTCGT GACTCANNNN NNNNNNNNNN NNNNNNNNNN
NNNNNNNNNN NNNNNNNNNN   60

NNNNNNNNNN NNNNNNTATA AANNNNNNNN NNNNNNNNNN
NNNNNNNNNN NNNNNNNNNN   120

NCTCTTAAGT GCAAGTGACT GCGAACATTT TTTTCGTTTG TTAGAATAAT
TCAAGAATCG   180

CTACCAATCA TGGATCCCG   199

(2) INFORMATION FOR SEQ ID NO: 4:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 45 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: double
     (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: YES

   (iv) ANTI-SENSE: NO

   (vi) ORIGINAL SOURCE:
     (A) ORGANISM: Pseudomonas putida

   (ix) FEATURE:
     (A) NAME/KEY: promoter
     (B) LOCATION:1..45
     (C) IDENTIFICATION METHOD: experimental
     (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
       /standard_name= "Artificial promoter library"
       /note= "A degenerated sequence specifying a mixture of
       artificial promoterscovering a wide range of expression in small
       steps Pseudomonas putida"

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

NNNNNNNNTT GRNNNNNNNN NNNNNNNNNN NTATRATNNN NNNNN
45

(2) INFORMATION FOR SEQ ID NO: 5:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 60 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: double
     (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:
    (A) NAME/KEY: promoter
    (B) LOCATION:4..60
    (D) OTHER INFORMATION:/standard_name= "Constitutional
        promoter"
        /label= Cp1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CATACCGGAG TTTATTCTTG ACAGTTCCAC CTCGGGTTGA TATAATATCT
CAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:
    (A) NAME/KEY: promoter
    (B) LOCATION:4..60
    (D) OTHER INFORMATION:/standard_name= "Constitutional

promoter"
/label= Cp10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CATGGCTTAG TTTATTCTTG ACAGGGTAGT ATCACTGTGA TATAATAGGA
CAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 59 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..59
        (D) OTHER INFORMATION:/standard_name= "Constitutional
            promoter"
            /label= Cp11

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CATAAGTGAG TTTATTCTTG ACCCGGACGC CCCCCTTTGA TATAATAAGT
AGTACTGTT   59

(2) INFORMATION FOR SEQ ID NO: 8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid

      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA (genomic)

  (iii) HYPOTHETICAL: YES

  (iv) ANTI-SENSE: NO

  (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Lactococcus lactis

  (ix) FEATURE:
      (A) NAME/KEY: promoter
      (B) LOCATION:4..60
      (D) OTHER INFORMATION:/standard_name= "Constitutional
          promoter"
          /label= Cp12

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CATATACAAG TTTATTCTTG ACACTAGTCG GCCAAAATGA TATAATACCT
GAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 9:

  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 60 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA (genomic)

  (iii) HYPOTHETICAL: YES

  (iv) ANTI-SENSE: NO

  (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Lactococcus lactis

  (ix) FEATURE:
      (A) NAME/KEY: promoter

(B) LOCATION:4..60
(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CATGCTTTAC TTTATTCTTG ACAAAACCAC CAGCTTTTGG TATAATACGT
GAGAACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:
(A) NAME/KEY: promoter
(B) LOCATION:4..60
(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CATGACGGAG TTTATTCTTG ACACAGGTAT GGACTTATGA TATAATAAAA
CAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 60 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:
    (A) NAME/KEY: promoter
    (B) LOCATION:4..60
    (D) OTHER INFORMATION:/standard_name= "Constitutional
       promoter"
       /label= Cp15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CATTACNTAG TTNATTCTTG ACAGAATTAC GATTCGCTGG TATAATATAT
CAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 58 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:
    (A) NAME/KEY: promoter
    (B) LOCATION:4..58
    (D) OTHER INFORMATION:/standard_name= "Constitutional
       promoter"
       /label= Cp16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CATTGTGTAG TTTATTCTTG ACAGCTATGA GTCAATTTGG TATAATAACA
GTACTCAG   58

(2) INFORMATION FOR SEQ ID NO: 13:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 59 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
       (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
       (A) NAME/KEY: promoter
       (B) LOCATION:4..59
       (D) OTHER INFORMATION:/standard_name= "Constitutional
         promoter"
         /label= Cp17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CATTCTGGAG TTTATTCTTG ACCGCTCAGT ATGCAGTGGT ATAATAGTAC
AGTACTGTT   59

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 58 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:
    (A) NAME/KEY: promoter
    (B) LOCATION:4..58
    (D) OTHER INFORMATION:/standard_name= "Constitutional
        promoter"
        /label= Cp18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CATTTTGCAG TTTATTCTTG ACATTGTGTG CTTCGGGTGT ATAATACTAA
GTACTGTT   58

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 58 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:
    (A) NAME/KEY: promoter
    (B) LOCATION:4..58
    (D) OTHER INFORMATION:/standard_name= "Constitutional
        promoter"
        /label= Cp19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CATCGCTTAG TTTTTCTTGA CAGGAGGGAT CCGGGTTGAT ATAATAGTTA
GTACTGTT   58

(2) INFORMATION FOR SEQ ID NO: 16:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..60
        (D) OTHER INFORMATION:/standard_name= "Constitutional
          promoter"
          /label= Cp2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CATTTGCTAG TTTATTCTTG ACATGAAGCG TGCCTAATGG TATATTACTT
GAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 17:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..60
        (D) OTHER INFORMATION:/standard_name= "Constitutional
           promoter"
           /label= Cp20

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CATGGGTGAG TTTATTCTTG ACAGTGCGGC CNGGGGCTGA TATCATAGCA
GAGTACTATT   60

(2) INFORMATION FOR SEQ ID NO: 18:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 59 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
     (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:
     (A) NAME/KEY: promoter
     (B) LOCATION:4..59
     (D) OTHER INFORMATION:/standard_name= "Constitutional
         promoter"
         /label= Cp21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CATTACCGAG TTTATTCTTG ACACCGTTTA TCGGGGTTGT ATAATACTAT
AGTACTGTT   59

(2) INFORMATION FOR SEQ ID NO: 19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

  (iii) HYPOTHETICAL: YES

   (iv) ANTI-SENSE: NO

   (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

   (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..60
        (D) OTHER INFORMATION:/standard_name= "Constitutional
            promoter"
            /label= Cp23

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CATGTAGGAG TTTATTCTTG ACAGATTAGT TAGGGGGTGG TATAATATCT
CAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 20:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 60 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA (genomic)

  (iii) HYPOTHETICAL: YES

  (iv) ANTI-SENSE: NO

  (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Lactococcus lactis

  (ix) FEATURE:
    (A) NAME/KEY: promoter
    (B) LOCATION:4..60
    (D) OTHER INFORMATION:/standard_name= "Constitutional
      promoter"
      /label= Cp24

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CATGGGTAAG TTTATTCTTC ACACTATCTG GGCCCGATGG TATAATAAGT
GACTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 21:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 59 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA (genomic)

  (iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:
    (A) NAME/KEY: promoter
    (B) LOCATION:3..59
    (D) OTHER INFORMATION:/standard_name= "Constitutional
        promoter"
        /label= Cp25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CTTTGGCAGT TTATTCTTGA CATGTAGTGA GGGGGCTGGT ATAATCACAT
AGTACTGTT   59

(2) INFORMATION FOR SEQ ID NO: 22:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..60
        (D) OTHER INFORMATION:/standard_name= "Constitutional
            promoter"
            /label= Cp26

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CATTCTACAG TTTATTCTTG ACATTGCACT GTCCCCCTGG TATAATAACT
ATACATGCAT   60

(2) INFORMATION FOR SEQ ID NO: 23:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 60 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: double
     (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: YES

   (iv) ANTI-SENSE: NO

   (vi) ORIGINAL SOURCE:
     (A) ORGANISM: Lactococcus lactis

   (ix) FEATURE:
     (A) NAME/KEY: promoter
     (B) LOCATION:4..60
     (D) OTHER INFORMATION:/standard_name= "Constitutional
      promoter"
      /label= Cp28

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CATGGGGCCG TTTATTCTTG ACAACGGCGA GCAGACCTGG TATAATAATA
TAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 24:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 59 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: double
     (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:
    (A) NAME/KEY: promoter
    (B) LOCATION:4..59
    (D) OTHER INFORMATION:/standard_name= "Constitutional
        promoter"
        /label= Cp29

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CATCGGTAAG TTATTCTTGA CATCTCAGGG GGGACGTGGT ATAATAACTG
AGTACTGTT 59

(2) INFORMATION FOR SEQ ID NO: 25:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..60
        (D) OTHER INFORMATION:/standard_name= "Constitutional
            promoter"
            /label= Cp3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CATCCTGTAG TTTATTCTTG ACACACGTNN TTAGCTGTGG TATAATAGGA
GAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 26:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..60
        (D) OTHER INFORMATION:/standard_name= "Constitutional
            promoter"
            /label= Cp30

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CATGACAGAG TTTATTCTTG ACAGTATTGG GTTACTTTGG TATAATAGTT
GAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 27:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:
    (A) NAME/KEY: promoter
    (B) LOCATION:4..60
    (D) OTHER INFORMATION:/standard_name= "Constitutional
       promoter"
       /label= Cp32

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CATACGGGAG TTTATTCTTG ACATATTGCC GGTGTGTTGG TATAATAACT
TAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 28:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 60 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
       (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
       (A) NAME/KEY: promoter
       (B) LOCATION:4..60
       (D) OTHER INFORMATION:/standard_name= "Constitutional
          promoter"

/label= Cp33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CATGTTGGAG TTTATTCTTG ACATACAATT ACTGCAGTGA TATAATAGGT
GAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 29:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION 4..60
        (D) OTHER INFORMATION:/standard_name= "Constitutional
            promoter"
            /label= Cp34

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CATCGCGAAG TTTATTCTTC ACACACCGCA GAACTTGTGG TATAATACAA
CAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 30:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 59 base pairs
        (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:
(A) NAME/KEY: promoter
(B) LOCATION:4..59
(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CATCATTAAG TTTATTCTTC ACATTGGCCG GAATTGTTGT ATAATACCTT
AGTACTGTT   59

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:
(A) NAME/KEY: promoter
(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional promoter"
/label= Cp38

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CATAGAGAAG TTTATTCTTG ACAGCTAACT TGGCCTTTGA TATAATACAT
GAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 32:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 60 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: double
     (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: YES

   (iv) ANTI-SENSE: NO

   (vi) ORIGINAL SOURCE:
     (A) ORGANISM: Lactococcus lactis

   (ix) FEATURE:
     (A) NAME/KEY: promoter
     (B) LOCATION:4..60
     (D) OTHER INFORMATION:/standard_name= "Constitutional promoter"
     /label= Cp39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

CATTGCGAAG TTTATTCTTG ACAGTACGTT TTTACCATGA TATAATAGTA
TAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 33:

   (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..60
        (D) OTHER INFORMATION:/standard_name= "Constitutional
            promoter"
            /label= Cp4

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GATGTTTTAG TTTATTCTTG ACACCGTATC GTGCGCGTGA TATAATCGGG
ATCCTTAAGA   60

(2) INFORMATION FOR SEQ ID NO: 34:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 59 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:
    (A) NAME/KEY: promoter
    (B) LOCATION:4
    (D) OTHER INFORMATION:/standard_name= "Constitutional
       promoter"
      /label= Cp40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CATAGAACAG TTTATTCTTG ACATTGAATA AGAAGGCTGA TATAATAGCC
AGTACTGTT   59

(2) INFORMATION FOR SEQ ID NO: 35:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 60 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA (genomic)

 (iii) HYPOTHETICAL: YES

  (iv) ANTI-SENSE: NO

  (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Lactococcus lactis

  (ix) FEATURE:
    (A) NAME/KEY: promoter
    (B) LOCATION:4..60
    (D) OTHER INFORMATION:/standard_name= "Constitutional
      promoter"
      /label= Cp41

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CATCCGCAAG TTTATTCTTG ACAGCTGAAT GTAGACGTGG TATAATAGTT
AAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 36:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 60 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA (genomic)

        (iii) HYPOTHETICAL: YES

        (iv) ANTI-SENSE: NO

        (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Lactococcus lactis

        (ix) FEATURE:
           (A) NAME/KEY: promoter
           (B) LOCATION:4..60
           (D) OTHER INFORMATION:/standard_name= "Constitutional
               promoter"
               /label= Cp42

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

CATTCGTAAG TTTATTCTTG ACACCTGAGA TGAGGCGTGA TATAATAAAT
AAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 37:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 59 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA (genomic)

        (iii) HYPOTHETICAL: YES

        (iv) ANTI-SENSE: NO

        (vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:
   (A) NAME/KEY: promoter
   (B) LOCATION:4..59
   (D) OTHER INFORMATION:/standard_name= "Constitutional
      promoter"
      /label= Cp44

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CATCGGGTAG TTTATTCTTG ACAATTAAGT AGAGCCTGAT ATAATAGTTC
AGTACTGTT   59

(2) INFORMATION FOR SEQ ID NO: 38:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 59 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: YES

   (iv) ANTI-SENSE: NO

   (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Lactococcus lactis

   (ix) FEATURE:
      (A) NAME/KEY: promoter
      (B) LOCATION:4..59
      (C) IDENTIFICATION METHOD: experimental
      (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
         /standard_name= "Constitutional promoter"
         /label= Cp5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CATGGGGGAG TTTATTCTTG ACATCATCTT CGTAGCCTGG TATACTACAT
GAGTATGTT   59

(2) INFORMATION FOR SEQ ID NO: 39:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 60 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: double
     (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: YES

   (iv) ANTI-SENSE: NO

   (vi) ORIGINAL SOURCE:
     (A) ORGANISM: Lactococcus lactis

   (ix) FEATURE:
     (A) NAME/KEY: promoter
     (B) LOCATION:4..60
     (D) OTHER INFORMATION:/standard_name= "Constitutional
       promoter"
       /label= Cp6

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CATGTGGGAG TTTATTCTTG ACACAGATAT TTCCGGATGA TATAATAACT
GAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 40:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 60 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: double
     (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: YES

   (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:
    (A) NAME/KEY: promoter
    (B) LOCATION:4..60
    (D) OTHER INFORMATION:/standard_name= "Constitutional
        promoter"
        /label= Cp7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

TATGCGGTAG TTTATTCTTG ACATGACGAG ACAGGTGTGG TATAATGGGT
CTAGATTAGG   60

(2) INFORMATION FOR SEQ ID NO: 41:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..60
        (D) OTHER INFORMATION:/standard_name= "Constitutional
            promoter"
            /label= Cp8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

CATTCTTTAG TTTATTCTTG ACAAACGTAT TGAGGACTGA TATAATAGGT
GAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 42:

  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 60 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA (genomic)

  (iii) HYPOTHETICAL: YES

  (iv) ANTI-SENSE: NO

  (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Lactococcus lactis

  (ix) FEATURE:
      (A) NAME/KEY: promoter
      (B) LOCATION:4..60
      (D) OTHER INFORMATION:/standard_name= "Constitutional
          promoter"
          /label= Cp9

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CATAGTCTAG TTTATTCTTG ACACGCGGTC CATTGGCTGG TATAATAATT
TAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 43:

  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 177 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Saccharomyces cerevisiae

(ix) FEATURE:
    (A) NAME/KEY: promoter
    (B) LOCATION:8..177
    (C) IDENTIFICATION METHOD: experimental
    (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
        /standard_name= "Yeast promoter"
        /label= Yp102

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GAATTCGTGA CTCAAACGGG TGGTCGACGG GTGGTTCCAA TTAATTGGCG
TCCCTCTTAT   60

AAAGGCGAGG GTACGTGCGA CAATTGGTAG AGCGAGCGGG GCTCTTAAGT
GCAAGTGACT   120

GCGAACATTT TTTTCGTTTG TTAGAATAAT TCAAGAATCG CTACCAATCA
TGGATCC   177

(2) INFORMATION FOR SEQ ID NO: 44:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 182 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Saccharomyces cerevisiae

    (ix) FEATURE:

        (A) NAME/KEY: promoter
        (B) LOCATION:8..181
        (C) IDENTIFICATION METHOD: experimental
        (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
            /standard_name= "Yeast promoter"
            /label= Yp112

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GAATTCGTGA CTCACGGCAT CTGATGGTTG ACCATAGTCA GGAACATTGT
GCTGGAGTTC   60

CTTGAGGAAT GAGTTATAAA ATGGGAGGTT GCGGCTAATG CCAGGCAGGA
GAGGAACCCT   120

CTTAAGTGCA AGTGACTGCA AACATTTTTT TCGTTTGTTG AATCGCTACC
AATCATGGAT   180

CC   182

(2) INFORMATION FOR SEQ ID NO: 45:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 191 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Saccharomyces cerevisiae

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:8..181
        (C) IDENTIFICATION METHOD: experimental
        (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
            /standard_name= "Yeast promoter"
            /label= Yp13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GAATTCGTGA CTCACTAGGC AGGTCACGTT GGCTCTTCGC GGCGCAGGTT
CGTATGCCGC   60

GCCGCCAGGG GCTTTATAAA GGTCGTCCTG GGTACAGTTG GGATGGCTCC
ACGTTTCGGC   120

TCTTAAGTGC AAGTGACTGC GAACATTTCG TTTGTTAGAA TAATTCAAGA
ATCGCTACCA   180

ATCATGGATC C   191

(2) INFORMATION FOR SEQ ID NO: 46:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 167 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Saccharomyces cerevisiae

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:8..167
        (C) IDENTIFICATION METHOD: experimental
        (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
            /standard_name= "Yeast promoter"
            /label= Yp15

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GAATTCGTGA CTCAGGGCCG TACTAAGTAG CTTTCGTATG CTATGCGGGG
TTTTATAAAT   60

CTTTGGGCCA TGGTCTTGCT GGAAAACACC TCTCTTAAGT GCAAGTGACT
GCGAACATTT   120

TTTTCGTTTG TTAGAATAAT TCAAGAATCG CTACCAATCA TGGATCC
167

(2) INFORMATION FOR SEQ ID NO: 47:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 191 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Saccharomyces cerevisiae

    (ix) FEATURE:
      (A) NAME/KEY: promoter
      (B) LOCATION:8..191
      (C) IDENTIFICATION METHOD: experimental
      (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
        /standard_name= "Yeast promoter"
        /label= Yp154

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GAATTCGTGA CTCACCGCTC GGGTGCAGGG CCAAGGCGGC GGAATGTGCG
GGGCGTTCTA   60

GCGCAATCGG GGTATAAATT TATAAGGAGG CTGCGGGTGC TAGTTTGTCT
AGTTTGACTC   120

TTAAGTGCAA GTGACTGCGA ACATTTTTCG TTTGTTAGAA TAATTCAAGA
ATCGCTACCA   180

ATCATGGATC C   191

(2) INFORMATION FOR SEQ ID NO: 48:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 195 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Saccharomyces cerevisiae

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:8..190
        (C) IDENTIFICATION METHOD: experimental
        (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
           /standard_name= "Yeast promoter"
           /label= Yp18

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

GAATTCGTGA CTCAGGATTA GCTATGCCGG TTGGGATAAG CGAACAACTG
GAGGTGAGAA   60

GCTTTTTGTC AGAATATAAA CCCGTTAGTC AGGGTTTGGT GGGATAGGGG
GTACTGTACC   120

TCTTAAGTGC AAGTGACTGC GAACATTTTT TTCGTTTGTT AGAATAATTC
AAGAATCGCT   180

ACCAATCATG GATCC   195

(2) INFORMATION FOR SEQ ID NO: 49:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 179 base pairs
        (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Saccharomyces cerevisiae

(ix) FEATURE:
    (A) NAME/KEY: promoter
    (B) LOCATION:8..179
    (C) IDENTIFICATION METHOD: experimental
    (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
        /standard_name= "Yeast promoter"
        /label= Yp183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GAATTCGTGA CTCACTAAGG GTTCGCCATT AACAGAATCG CTGGTAGAAC
ATCGGTAGTT   60

AGGCACCCGA GTATAAACAG GCGGACCCCT CACGGATATC AGCTGATAGT
GCGAGCCTCA   120

ATGCGAACAT TTTTTTCGTT TGTTAGAATA ATTCAAGAAT CGCTACCAAT
CATGGATCC   179

(2) INFORMATION FOR SEQ ID NO: 50:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 195 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Saccharomyces cerevisiae

(ix) FEATURE:
    (A) NAME/KEY: promoter
    (B) LOCATION:8..190
    (C) IDENTIFICATION METHOD: experimental
    (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
        /standard_name= "Yest promoter"
        /label= Yp190

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

GAATTCGTGA CTCAGTATCC ACGGGTGTTT GAGGGCTGGT CGCAGGTTAG
CAGGCGAGGG   60

CGGGTGGTTA CGGCTATAAA TGAGTGTTTG CAGCCGGGTA CGGGCGTACG
AGTAGTGATC   120

TCTTAAATGC AAGTGACTGC GAACATTTTT TTCGTTTGTT AGAATAATTC
AAGAATCGCT   180

ACCAATCATG GATCC   195

(2) INFORMATION FOR SEQ ID NO: 51:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 193 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Saccharomyces cerevisiae

    (ix) FEATURE:
        (A) NAME/KEY: promoter

(B) LOCATION:8..189
(C) IDENTIFICATION METHOD: experimental
(D) OTHER INFORMATION:/evidence= EXPERIMENTAL
/standard_name= "Yest promoter"
/label= Yp191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GAATTCGTGA CTCAATGCTG CGGGCGGCAG GAGTCTGGTG TAACTTCCCA
TTTTGAGTGA   60

AAGACAGACC ATCTATAAAC ATTTGGTGGG CAAAGTGGCC TGGCGGATTT
GTTTGGACTC   120

TTAAGTGAAA GTGACTGCGA ACATTTTTTT CGTTTGTTAG AATAATTCAA
GAATCGCTAC   180

CAATCATGGA TCC   193

(2) INFORMATION FOR SEQ ID NO: 52:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 166 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Saccharomyces cerevisiae

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:8..166
        (C) IDENTIFICATION METHOD: experimental
        (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
            /standard_name= "Yeast promoter"
            /label= Yp192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

GAATTCGTGA CTCACTTAAG GCTACTGCGG AAGTTTAGAT CTAAGGTCGG
AAATAATTTA   60

GAAAATTACG ACATTATAAA TAGCGGAGAG GCCAGGTGAT GGGCACCATT
GTGGGGGGGC   120

TCTTAATTGT TAGAATAATT CAAGAATCGC TACCAATCAT GGATCC
166

(2) INFORMATION FOR SEQ ID NO: 53:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 195 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Saccharomyces cerevisiae

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:8..190
        (C) IDENTIFICATION METHOD: experimental
        (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
           /standard_name= "Yeast promoter"
           /label= Yp212

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GAATTCGTGA CTCAGTCGCC CGCAAGATGG GATGGTGCAT TTTAAACACC
CGAATTATAC   60

TCGTCAACTT ATAGTATAAA CGGAACGCGA CGATACGTTC TAGTTTTCGG
CGAAGTCGAC   120

TCTTAAGTGC AAGTGACTGC GAACATTTTT TTCGTTTGTT AGAATAATTC
AAGAATCGCT   180

ACCAATCATG GATCC   195

(2) INFORMATION FOR SEQ ID NO: 54:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 188 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Saccharomyces cerevisiae

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:8..183
        (C) IDENTIFICATION METHOD: experimental
        (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
           /standard_name= "Yeast promoter"
           /label= Yp24

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

GAATTCGTAC TCACGACAGC GTTATGACTT CGAGGACCAG CTACTTCCGG
TCGCGTACTA   60

GTTTTTACCT GTATAAACTT TGCTACCGCT GGGCCTTGGT GGTGCTGTCC
CGCTCTTAAG   120

TGCAAGTGAC TGCGAACATT TTTTTCGTTT GTTACAATAA TTCAAGAATC
GCTACCAATC   180

ATGGATCC   188

(2) INFORMATION FOR SEQ ID NO: 55:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 195 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Saccharomyces cerevisiae

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:8..190
        (C) IDENTIFICATION METHOD: experimental
        (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
            /standard_name= "Yeast promoter"
            /label= Yp435

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GAATTCGTGA CTAAATGGAT AAGGTTATCG CCATCACGGA GTCTTCTCTC
ACGTCTGGAG   60

CAGAGGCTAG ACCTTATAAA TTATACATGG TGGGAGAGGC GATAGTCTTT
AGAGACGTGC   120

TCTTAAGTGC AAGTGACTGC GAACATTTTT TTCGTTTGTT AGAATAATTC
AAGAATCGCT   180

ACCAATCATG GATCC   195

(2) INFORMATION FOR SEQ ID NO: 56:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 189 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Saccharomyces cerevisiae

(ix) FEATURE:
    (A) NAME/KEY: promoter
    (B) LOCATION:8..184
    (C) IDENTIFICATION METHOD: experimental
    (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
       /standard_name= "Yeast promoter"
       /label= Yp68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

GAATTCGTGA CTCACAAGAA TGTGGGCGGG TCGTTAAACT GAGCCTGGAC
ACCTTGGCTG   60

CGTCGCTTTC GTATAAAGAT CTTAGAGCTG TGGAGTCTGG GTCGAGTGGC
CAGCTCTTAA   120

ATGCAAGTGA CTGCGAACAT TTTTTTCGTT TGTTAGAATA ATTCAAGAAT
CGCTACCAAT   180

CATGGATCC   189

(2) INFORMATION FOR SEQ ID NO: 57:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 195 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Saccharomyces cerevisiae

(ix) FEATURE:
    (A) NAME/KEY: promoter
    (B) LOCATION:8..190
    (C) IDENTIFICATION METHOD: experimental
    (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
        /standard_name= "Yeast promoter"
        /label= Yp89

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

GAATTCGTGA CTCACTCGGA AGATTGGGTT TACGATTAGG ATGGCGCGGC
AGAACCGGGG   60

GGGATTCCCT TCTATATAAA GGGTTCCGAT ACTACGTGCT GCGGACGGCC
GATCGAGTTA   120

TCTTAAGTGC AAGTGACTGC GAAAATTTTT TTCGTTTGTT AGAATAATTC
AAGAATCGCT   180

ACCAATCATG GATCC   195

(2) INFORMATION FOR SEQ ID NO: 58:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 176 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Saccharomyces cerevisiae

    (ix) FEATURE:

(A) NAME/KEY: promoter
(B) LOCATION:8..171
(C) IDENTIFICATION METHOD: experimental
(D) OTHER INFORMATION:/evidence= EXPERIMENTAL
    /standard_name= "Yeast promoter"
    /label= Yp96

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GAATTCGTGA CTCATCTAGT GAGAGGAGCC GTGGTATCTT GTGTCACCAC
CAGGGGAAAA   60

TAATGGCAGG GGTGTATAAA TGGTCGAGTA GTCGCGACCC ACGCTGCAAG
GCAAGGAACT   120

CTTAAATTTT TTTCGTTTGT TAGAATAATT CAAGAATCGC TACCAATCAT
GGATCC   176